

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 17, 2003, 16:09:08 ; Search time 11 Seconds

(without alignments)  
912.479 Million cell updates/sec

Title: US-09-978-309a-74

Perfect score: 1195  
Sequence: 1 QEKYDSMWSLEDVTAQFES.....KKKQSETKLOELNKVLGIK 242

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08  
Maximum Match 1008

Listing first 45 summaries

Database: SwissProt\_40.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	1193	99.8	724 1	HMNR_HUMAN
2	913	76.4	794 1	HMNR_MOUSE
3	897	75.1	498 1	HMNR_RAT
4	191	16.0	976 1	SCPL_HUMAN
5	185.5	15.5	1790 1	USOL_YEAST
6	182.5	15.3	1938 1	MYH4_YEAST
7	181.5	15.2	1940 1	MYH4_RABIT
8	180.5	15.1	1941 1	MYH3_RAT
9	179.5	15.0	1938 1	MYH2_HUMAN
10	179.5	15.0	1938 1	MYSS_CHICK
11	179.5	15.0	1938 1	MYH4_HUMAN
12	178.5	14.9	1939 1	MEP1_LYCES
13	178.5	14.9	1940 1	MYH1_HUMAN
14	176.5	14.8	845 1	SCPL_MESAU
15	176.5	14.8	1937 1	MYH8_HUMAN
16	176.5	14.8	1940 1	MYH3_CHICK
17	175	14.6	993 1	SCPL_MOUSE
18	172.5	14.4	864 1	RA50_SULISO
19	172.5	14.4	865 1	MYSP_RABIT
20	171.5	14.4	1935 1	MYSS_CYCMA
21	171	14.3	886 1	MYSS_CYPCA
22	169	14.1	2230 1	GOG4_HUMAN
23	167	14.0	2245 1	MYSJ_DICDI
24	166.5	13.9	1102 1	MYSS_RABIT
25	166.5	13.9	1102 1	MYSS_CHICK
26	165.5	13.8	879 1	RA50_SULTO
27	162.5	13.6	1938 1	MYH6_MOUSE
28	162.5	13.6	1939 1	MYH6_HUMAN
29	162	13.6	1935 1	MYH7_PIG
30	161.5	13.5	1938 1	MYH6_RAT
31	161.5	13.5	1939 1	MYH6_MESAU
32	161	13.5	866 1	MYSP_SCHUA
33	161	13.5	1935 1	MYH7_HUMAN

34	160.5	13.4	1286 1	CTRO_HUMAN	014578 homo sapien
35	160	13.4	1679 1	YIO9_YEAST	P40457 saccharomyc
36	160	13.4	1935 1	MYH7_RAT	P02564 rattus norv
37	160	13.4	1978 1	MYH8_CHICK	P10587 gallus gall
38	159.5	13.3	1597 1	CTRO_MOUSE	P49025 mus musculu
39	159.5	13.3	1938 1	MYH8_HUMAN	O9ukx3 homo sapien
40	158	13.2	978 1	RA50_AOUAE	O67124 aquilex aeo
41	158	13.2	1203 1	SCPE_XENLA	P50533 xenopus lae
42	157.5	13.2	997 1	SCPL_RAT	O03410 rattus norv
43	156.5	13.1	886 1	RA50_ARCFU	O29230 archaeglob
44	156.5	13.1	1325 1	GL60_MOUSE	P55937 mus musculu
45	155.5	13.0	1957 1	YD86_SCHPO	Q10411 schizosacch

## ALIGNMENTS

RESULT 1	ID	HMNR_HUMAN	STANDARD:	PRT:	724 AA.
AC	075330	092767			
DT	30-MAY-2000	(Rel. 39, Created)			
DT	30-MAY-2000	(Rel. 39, Last sequence update)			
DT	15-JUN-2002	(Rel. 41, Last annotation update)			
DE	Hyaluronan mediated motility receptor (intracellular hyaluronic acid binding protein) (Receptor for hyaluronan-mediated motility) (CD168 antigen).				
DE	antigen).				
GN	HMNR OR IHABP OR RHAMM.				
OS	Homo sapiens (human).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
OX	NCBI_TaxID:9606;				
RN	[1]				
RP	SEQUENCE FROM N.A., ALTERNATIVE SPLICING, AND CHARACTERIZATION.				
RC	TISSUE=breast carcinoma;				
RA	MEDLINE=98264864; PubMed=9601098;				
RA	Assmann V., Marshall J.F., Fieber C., Hofmann M., Hart I.R.;				
RT	"The human hyaluronan receptor RHAMM is expressed as an intracellular protein in breast cancer cells.";				
RL	J. Cell Sci. 111:1685-1694(1998).				
RP	[2]				
RC	SEQUENCE FROM N.A.				
RA	TISSUE=breast;				
RA	MEDLINE=97045829; PubMed=8890751;				
RT	Wang C., Entwistle J., Hou G., Li O., Turley E.A.;				
RT	"The characterization of a human RHAMM cDNA: conservation of the hyaluronan-binding domains.";				
RL	Gene 174:299-306(1996).				
CC	- FUNCTION: INVOLVED IN CELL MOTILITY. WHEN HYALURONAN BINDS TO HMNR, THE PHOSPHORYLATION OF A NUMBER OF PROTEINS, INCLUDING THE FOCAL ADHESION KINASE OCCURS. MAY ALSO BE INVOLVED IN CELLULAR TRANSFORMATION AND METASTASIS FORMATION, AND IN REGULATING EXTRACELLULAR-REGULATED KINASE (ERK) ACTIVITY.				
CC	- SUBUNIT: SUBUNIT OF THE HARC COMPLEX.				
CC	- SUBCELLULAR LOCATION: CELL SURFACE AND CYTOPLASMIC (BY SIMILARITY).				
CC	- ALTERNATIVE PRODUCTS: 2 ISOFORMS: A (SHOWN HERE) AND B; ARE PRODUCED BY ALTERNATIVE SPLICING.				
CC	- TISSUE SPECIFICITY: EXPRESSED IN BREAST CANCER CELL LINES AND IN NORMAL BREAST TISSUE.				
CC	- DATABASE: NAME=PROW; NOTE=PROW 2:76-84(2001);				
CC	WWW="http://www.ncbi.nlm.nih.gov/prov/guide/80286666.g.htm".				
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CC	EMBL: AF032862; AAC32548.1;				
DR	EMBL: U29343; AAC52049.1;				

DR Genew; HGNC:5012; HMMR.  
 DR MW; 600936; -  
 KW Hyaluronic acid; Alternative splicing; Repeat: Glycoprotein; Antigen.  
 FT DOMAIN 635 645 HYALURONIC ACID-BINDING (POTENTIAL).  
 FT CARBOHYD 657 666 HYALURONIC ACID-BINDING (POTENTIAL).  
 FT CARBOHYD 133 133 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 477 477 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 567 567 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 588 588 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT VARSPLIC 75 90 MISSING (IN ISOFORM B).  
 FT CONFLICT 75 75 K -> KR (IN REF. 2).  
 FT CONFLICT 103 103 S -> R (IN REF. 2).  
 FT CONFLICT 277 277 E -> D (IN REF. 2).  
 FT CONFLICT 298 298 K -> T (IN REF. 2).  
 FT CONFLICT 322 322 K -> E (IN REF. 2).  
 FT CONFLICT 330 332 OER -> REH (IN REF. 2).  
 SQ SEQUENCE 724 AA; 84031 MW; EA68AD6D2A626926 CRC64;

Query Match 99.8%; Score 1193; DB 1; Length 724;  
 Best Local Similarity 99.6%; Pred. No. 6.5e-54;  
 Matches 241; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QERYDSWVQSLIEDVTAQFESYKALTSIEDLKLNSLOEKAKAKNAEDVOHQLIAT 60  
 DB 442 QERYDSWVQSLIEDVTAQFESYKALTSIEDLKLNSLOEKAKAKNAEDVOHQLIAT 501  
 QY 61 ESSNOEYVRMLDLQTKSAKETEIKETYSFLQKTTDLONOLKOEEDFRKOLEDEGR 120  
 DB 502 ESSNOEYVRMLDLQTKSAKETEIKETYSFLQKTTDLONOLKOEEDFRKOLEDEGR 561  
 QY 121 KAEKENTTALTEINKNRLLYEELYNKTRPQIOLDAFEVEKQALLNENGAEOELNKI 180  
 DB 562 KAEKENTTALTEINKNRLLYEELYNKTRPQIOLDAFEVEKQALLNENGAEOELNKI 621  
 QY 181 RDSYAKLLGHONLKOKIKHYVKKKDNSQKSEVSKIRCOLAKKSETRKLOEELNKVIG 240  
 DB 622 RDSYAKLLGHONLKOKIKHYVKKKDNSQKSEVSKIRCOLAKKSETRKLOEELNKVIG 681  
 QY 241 IK 242  
 DB 682 IK 683

RESULT 2  
 HMMR MOUSE STANDARD; PRT; 794 AA.  
 ID HMMR MOUSE  
 AC 000547;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE Hyaluronan mediated motility receptor (Intracellular hyaluronate acid binding protein) (Receptor for hyaluronan-mediated motility).  
 GN HMMR OR IHABP OR RHAMM.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND SUBCELLULAR LOCATION.  
 RC TISSUE=Lung;  
 RA MEDLINE=98264863; PubMed=9601097;  
 RA Hofmann M., Fieber C., Assmann V., Goettlicher M., Sleeman J.,  
 RA Plug R., Howells N., von Stein O., Ponta H., Herrlich P.;  
 RT "Identification of IHABP, a 95 kDa intracellular hyaluronate binding protein.";  
 RL J. Cell Sci. 111:1673-1684(1998).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Zhao Y., Zhang S., Turley E.;  
 RL Submitted (Jul-1998) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE OF 1-183 FROM N.A., AND TISSUE SPECIFICITY.  
 RC STRAIN=129/Sv;

RX MEDLINE=99107769; PubMed=98893113;  
 RA Fieber C., Plug R., Sleeman J., Dall P., Ponta H., Hofmann M.;  
 RT "Characterization of the murine gene encoding the intracellular  
 RL hyaluronan receptor IHABP.";  
 RL Gene 226:41-50(1999).  
 RN [4]  
 RP SEQUENCE OF 164-794 FROM N.A., AND ALTERNATIVE SPLICING;  
 RC STRAIN=BALB/C; TISSUE=Fibroblast;  
 RX MEDLINE=96011639; PubMed=7590272;  
 RA Entwistle J., Zhang S., Yang B., Wong C., Li Q., Hall C.L., A.J.;  
 RA Mowat M., Greenberg A.H., Turley E.A.;  
 RT "Characterization of the murine gene encoding the hyaluronan receptor  
 RL RHAMM.";  
 RL Gene 163:233-238(1995).  
 RN [5]  
 RP SEQUENCE OF 318-794 FROM N.A., AND CHARACTERIZATION.  
 RC STRAIN=BALB/C;  
 RX MEDLINE=92293690; PubMed=1376732;  
 RA Hardwick C., Hoare K., Owens R., Hohn H.P., Hook M., Moore D.,  
 RA Clippes V., Austen L., Nance D.M., Turley E.A.;  
 RT "Molecular cloning of a novel hyaluronan receptor that mediates tumor  
 RL cell motility.";  
 RL J. Cell Biol. 117:1343-1350(1992).  
 RN [6]  
 RP CHARACTERIZATION.  
 RX MEDLINE=94308286; PubMed=7518470;  
 RA Hall C.L., Wang C., Lange L.A., Turley E.A.;  
 RT "Hyaluronan and the hyaluronan receptor RHAMM promote focal adhesion  
 RL turnover and transient tyrosine kinase activity.";  
 RL J. Cell Biol. 126:575-586(1994).  
 RN [7]  
 RP ERK REGULATION, AND SUBCELLULAR LOCATION.  
 RX MEDLINE=98225222; PubMed=9556628;  
 RA Zhang S., Chang M.C., Zylka D., Turley S., Harrison R., Turley E.A.;  
 RT "The hyaluronan receptor RHAMM regulates extracellular-regulated  
 RL kinase.";  
 RL J. Biol. Chem. 273:11342-11348(1998).  
 RN [8]  
 RP REVIEW.  
 RX MEDLINE=99059494; PubMed=9845361;  
 RA Hofmann M., Assmann V., Fieber C., Sleeman J.P., Moll J., Ponta H.,  
 RA Hart I.R., Herrlich P.;  
 RT "Problems with RHAMM: a new link between surface adhesion and  
 RL oncogenesis?";  
 RL Cell 95:591-592(1998).  
 CC -1- FUNCTION: INVOLVED IN CELL MOTILITY. WHEN HYALURONAN BINDS TO  
 CC HMMR, THE PHOSPHORYLATION OF A NUMBER OF PROTEINS, INCLUDING THE  
 CC FOCAL ADHESION KINASE OCCURS. MAY ALSO BE INVOLVED IN CELLULAR  
 CC TRANSFORMATION AND METASTASIS FORMATION, AND IN REGULATING  
 CC EXTRACELLULAR-REGULATED KINASE (ERK) ACTIVITY.  
 CC -1- SUBUNIT: SUBUNIT OF THE HARC COMPLEX.  
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS: RHAMM1V4 (SHOWN HERE) AND  
 CC RHAMM1. ARE PRODUCED BY ALTERNATIVE SPLICING.  
 CC -1- TISSUE SPECIFICITY: UBQUITOUSLY EXPRESSED.  
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 CC  
 DR EMBL; AF031932; AAC12655.1;  
 DR EMBL; AF079222; AAD08670.1;  
 DR EMBL; AJ005919; CAA06768.1;  
 DR EMBL; AJ005920; CAA06768.1;  
 DR EMBL; AJ005921; CAA06768.1; JOINED  
 DR EMBL; AJ005922; CAA06768.1; JOINED  
 DR EMBL; AJ005923; CAA06768.1; JOINED  
 DR EMBL; AJ005924; CAA06768.1; JOINED  
 DR EMBL; X64550; CAA45849.1;

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RA Savani R. C., Hou G.;
FL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
CC
CC -I- FUNCTION: INVOLVED IN CELL MOTILITY. WHEN HYALURONAN BINDS TO
CC HMMR, THE PHOSPHORYLATION OF A NUMBER OF PROTEINS, INCLUDING THE
CC FOCAL ADHESION KINASE OCCURS. MAY ALSO BE INVOLVED IN CELLULAR
CC TRANSFORMATION AND METASTASIS FORMATION, AND IN REGULATING
CC EXTRACELLULAR-REGULATED KINASE (ERK) ACTIVITY (BY SIMILARITY).
CC -I- SUBUNIT: SUBUNIT OF THE HARC COMPLEX.
CC -I- SUBCELLULAR LOCATION: CELL SURFACE AND CYTOPLASMIC (BY
CC SIMILARITY).
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CC
CC DR EMBL: U87983; AAB47997.1; -.
CC
CC KW Hyaluronic acid; Repeat; Glycoprotein.
CC FT DOMAIN 420 430
CC FT HYALURONIC ACID-BINDING (POTENTIAL).
CC FT DOMAIN 442 451
CC FT HYALURONIC ACID-BINDING (POTENTIAL).
CC FT CARBOHYD 262 262
CC FT N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 302 302
CC FT N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 483 483
CC FT N-LINKED (GLCNAC. . .) (POTENTIAL).
CC SO SEQUENCE 498 AA; 57858 MW; 36037C79BD5C2A70 CRC64;
Query Match 75.1%; Score 897; DB 1; Length 498;
Best Local Similarity 74.4%; Pred. Num. 9; 4.2e-39;

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Query Match      75.1%; Score 897; DB 1; Length 490;
Best Local Similarity 74.4%; Pred. No. 4.2e-39;
Matches 180; Conservative 20; Mismatches 42; Indels 0; Gaps 0;

1 QEKYSMWSLEDVTAQEFESYKALTAASEIDKLKLENSLSQEKRAAKAGNAEDVQHILAT 60
|||||

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D0	22	QENSYIAOTLKHVYAOLESYSSFLKTEIEDLKLENTLLOEKVMAAEKRRVEDVOOOIITTA	286
QY	61	ESSNOEYVMM,LDLOTKSALKEETEKEITVSPFIKOTIDLOAQLOKOOEEDFPKOLEDEGR	1206
D0	287	ESINOEYXAVYDOLNONSSTLKAELEKEITSSYLEKITIDLOAQLOKQONEDFPKOLEEBCAK	3466
QY	121	KAEKENTTAELEBEINKWR,LYEEELYNKTRPFOIOLDAFEVEKQALLNENHGAOEOULNKI	1806
D0	347	MEKEEAVYELTMEINIKWRL,LYEEELYDYTKRPFQOOLDFAEAKOALLNENHGAOTEOULSKI	4066
QY	181	ROSYAKTLGHONL,OKIRKHVYTLKQENSO,LTSEVSKLRCOLAKKROSETKIOEELN,VLG	2406
D0	407	RDSYAO,LLSHONL,KOKIRKHVYALKDENSO,LSSEVSKLSQ,LAKKRONELRLOGLDELKALG	4666
QY	241	IK 242	
D0	467	IR 468	

RT	SCPI_HUMAN	STANDARD:	PRF:	976 AA.
ID	SCPI_HUMAN			
AC	O15431; O14963;			
DT	15-JUL-1998 (Rel. 36	Created)		
DT	15-JUL-1998 (Rel. 36;	Last sequence update)		
DT	16-OCT-2001 (Rel. 40;	Last annotation update)		
DE	Synaptonemal complex protein 1 (SCP-1 protein).			
GN	SCPI OR SCPI.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI:TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Testis;			
RC	MEDLINE=97224467; PubMed=9119375;			
RA	Meuwissen R.L.J., Meerts I., Hoovers J.M.N., Leschot N.J.,			
RA	Heyling C.;			
RT	"Human synaptonemal complex protein 1 (SCPI): isolation and			

RT characterization of the cDNA and chromosomal localization of the gene." ;  
 RT Genomics 39:377-384(1997).  
 [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-Testis;  
 RA MEDLINE=98037449; PubMed=9371398;  
 RA Kondoh N., Nishina Y., Tsuchida J., Koga M., Tanaka H., Uchida K.,  
 RA Inazawa J., Taketo M., Nozaki M., Nojima H., Matsunaga K., Namiki M.,  
 RA Okuyama A., Nishimune Y.,  
 RT "Assignment of synaptonemal complex protein 1 (SCP1) to human  
 RT chromosome 1p13 by fluorescence in situ hybridization and its  
 RT expression in the testis."  
 RT Cytogenet. Cell Genet. 78:103-104(1997).  
 CC -1- FUNCTION: MAJOR COMPONENT OF THE TRANSVERSE FILAMENTS OF  
 CC SYNAPTONEMAL COMPLEXES (SCS), FORMED BETWEEN HOMOLOGOUS  
 CC CHROMOSOMES DURING MEIOTIC PROPHASE.  
 CC -1- SUPRACELLULAR LOCATION: NUCLEAR. IN TRIPARTITE SEGMENTS OF  
 CC SYNAPTONEMAL COMPLEXES, BETWEEN LATERAL ELEMENTS IN THE NUCLEUS,  
 CC FOUND ONLY WHERE THE CHROMOSOME CORES ARE SYNAPSED. ITS N-TERMINUS  
 CC IS FOUND TOWARDS THE CENTRE OF THE SYNAPTONEMAL COMPLEX WHILE THE  
 CC C-TERMINUS EXTENDS WELL INTO THE LATERAL DOMAIN OF THE  
 CC SYNAPTONEMAL COMPLEX (BY SIMILARITY).  
 CC -1- TISSUE SPECIFICITY: TESTIS.  
 CC -1- DOMAIN: CONSISTS OF AN ALPHA-HELICAL STRETCH OF 700 AA RESIDUES,  
 CC FLANKED BY N- AND C-TERMINAL GLOBULAR DOMAINS, THE C-TERMINAL  
 CC DOMAIN HAS DNA-BINDING CAPACITY (BY SIMILARITY).  
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 CC  
 DR EMBL: X95654; CA64956.1;  
 DR EMBL: D67035; BAA2586.1;  
 DR Genew: HGNC:11487; SYCP1.  
 DR MIM: 602162;  
 KW Nuclear protein; Meiosis; Cell division; Phosphorylation;  
 KW DNA-binding; Coiled coil.  
 FT DOMAIN 12 100  
 FT DOMAIN 107 798  
 FT DOMAIN 117 120  
 FT DOMAIN 679 682  
 FT DOMAIN 880 883  
 FT DOMAIN 961 969  
 FT DOMAIN 46 46  
 FT CONFLICT 106 106  
 FT CONFLICT 153 153  
 FT CONFLICT 161 161  
 FT CONFLICT 168 168  
 FT CONFLICT 216 216  
 FT CONFLICT 225 226  
 FT CONFLICT 350 350  
 FT CONFLICT 360 360  
 FT CONFLICT 400 401  
 FT CONFLICT 406 406  
 FT CONFLICT 415 415  
 FT CONFLICT 449 449  
 FT CONFLICT 483 510  
 FT CONFLICT 516 528  
 FT CONFLICT 549 549  
 FT CONFLICT 560 560  
 FT CONFLICT 805 805  
 FT CONFLICT 941 941  
 FT SEQUENCE 976 AA; 114069 MW; 8BA81D042AC2696B CRC64;  
 Query Match 16.08; Score 191; DB 1; Length 976;  
 Best Local Similarity 23.38; Pred. No. 0.0042;

Matches 79; Conservative 53; Mismatches 103; Indels 104; Gaps 12;  
 QY 1 OEKIDSWOVEDVTAOFESYKALTA---ETEDLK-----LENSISLOKAAKAG 47  
 Db 402 EDOLKILTMELQKSSSELEEMTKLTNNKEVELELKVKYIGKEKTLTYNNKF-ETIAEEL 460  
 QY 48 KNAE-----DVQHOIATRESSNOEYVRRLDLOTK--SALKETET---- 85  
 Db 461 KGTBELIGLQAREKEVHDLTDTLTATTSOYYSKEVNDKTELENEKTKNELTSHC 520  
 QY 86 -----KEITVSFLQKTTDLONLQOEEDFRLODEBGRKKEKENTTAELFEELNK 138  
 Db 521 NKLSLENELT-----QETSDWTLKQOEDINNNKOEEMKQIENLODETOLNEL 576  
 QY 139 RLALBELYNKRPPOIOLDAF-----VEKQALLNENGAOEOEL 177  
 Db 577 EYVEELKQKRDVEKCKLDSEENCNNILRKOVENKRYIELOQENKALKKGTAEKOL 636  
 QY 178 N-----KIRDSYA-----KILGHONLQKIKHYVKKLQENSOLK 211  
 Db 637 NVYEIKYKMLELESARKQFGETDTYQKEIEDKISSENLLEVEKAKVIADDAVKI 696  
 QY 212 SEVSKLRQ-----LAKKQSETKLOEELNKYGI 241  
 Db 697 KEIDK-RCQKIAEMVALMEKHKHQYDKIIIEBDSGL 734  
 RESULT 5  
 USOL\_YEAST STANDARD; PRT; 1790 AA.  
 ID USOL\_YEAST  
 AC P25386;  
 DT 01-MAY-1992 (Rel. 22, Created)  
 DT 01-MAY-1992 (Rel. 22, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Intracellular protein transport protein USOL.  
 GN USOL OR INT1 OR YDL058W.  
 OS Saccharomyces cerevisiae (Baker's yeast).  
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.  
 OX NCBI\_TaxID=4932;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=X2180-1A;  
 RX MEDLINE=91185402; PubMed=2010462;  
 RA Nakajima H., Hirata A., Ogawa Y., Yonehara T., Yoda K.,  
 RA Yamasaki M.,  
 RT "A cytoskeleton-related gene, usol1, is required for intracellular  
 RT protein transport in Saccharomyces cerevisiae."  
 RT J Cell Biol. 113:245-260(1991).  
 RL [2]  
 RP SEQUENCE OF 782-1790 FROM N.A.  
 RA Hostetter M.K., Herman D.J., Bendel C.M., McClellan M., Tao N.,  
 RA Kendrick K.E.,  
 RL Submitted (FEB-1993) to the EMBL/GenBank/DBJ databases.  
 RP [3]  
 RP SEQUENCE OF 1-8 FROM N.A.  
 RA Bai Y., Symington L.S.,  
 RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: REQUIRED FOR PROTEIN TRANSPORT FROM THE ER TO THE GOLGI  
 CC COMPLEX.  
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC. ASSOCIATED WITH INTRACELLULAR  
 CC MEMBRANES. PROBABLY PRESENT ON VESICLES OPERATIONAL BETWEEN THE  
 CC ER AND THE GOLGI COMPLEX.  
 CC -1- DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, COMPOSED  
 CC OF AN HEPTAPEPTIDE REPEAT PATTERN CHARACTERISTIC OF ALPHA-HELICAL  
 CC COILED COILS. MAY FORM FILAMENTOUS STRUCTURES IN THE CELL.  
 CC -1- SIMILARITY: BELONGS TO THE VDP/USOL/YBL047C FAMILY.  
 CC  
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CC EMBL: X54378; CAA38253.1; -

DR EMBL: L03188; AAB00143.1; -

DR EMBL: U53668; AAB66559.1; -

DR PIR: A38455; A38453.

DR SDD: S0002216; USOL.

DR InterPro: IPR002017; Spectrin.

KW Transport; Protein transport; Golgi stack; Cytoskeleton; Coiled coil.

FT DOMAIN 1 726

FT DOMAIN 725 1790

FT DOMAIN 465 1790

FT DOMAIN 991 1790

FT DOMAIN 1172 1786

FT DOMAIN 847 847

FT CONFLICT 924 924

FT CONFLICT 1253 1253

FT CONFLICT 1319 1319

FT CONFLICT 1461 1461

FT CONFLICT 1581 1581

FT CONFLICT 1600 1600

FT CONFLICT 1661 1661

FT CONFLICT 1772 1772

SO SEQUENCE 1790 AA; 206424 MW; 6CE2B216E9FD4818 CRC64;

Query Match 15.5%; Score 185.5; DB 1; Length 1790;

Best Local Similarity 25.3%; Pred. No. 0.015;

Matches 72; Conservative 53; Mismatches 101; Indels 59; Gaps 10;

QY 5 DDMOSLEEVTAQFESYKALITNS-----EIEDKLKLENSLSLOEKAKAGKNAEDVQHOI 57

DB 1148 ESLEKEHEDLAOLKKEEIOANKEROYNEISQLEDEITSYQOENESIKKKNDELEGV 1207

QY 58 LATSSNOEYVM-----LIDLQTKSAKETEIEITY-----SLQKITDLOQL 103

DB 1208 KAKKSTSEBQSLKSEIDLALQIKELKKNETNEASLESIKSVSETVIKELQDEDC 1267

QY 104 KOQEDFRKQLEDEGRKAKENTTAELTEIEINKRLLYEELYNKTKPROIOLDAF----- 159

DB 1268 NKEKEV--SELEDKLAKSEDKSKYLELOKESK-----IKEEDATNTTEIKLOLEKTNIS 1323

QY 160 -----EVE-----KQALLNEGAAQEOQLNKIR-----DSYAKLGH-----QNL 193

DB 1334 KAKESESELRLKTSSEERKNAEOLKNEIKNOAQEKERKLLNBSSTTTQEX 1383

QY 194 KOKIK-----HYVKKLDENSQKSEVSKRLCOQAKKROSETKLOEE 234

DB 1384 SEKITLDELIRLQENELAKELIDNTRSELEKVSINDELLEE 1428

RESULT 6

MYH4\_RABIT STANDARD: PRT: 1938 AA.

AC 028641:

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Myosin heavy chain, skeletal muscle, juvenile.

OS Oryctolagus cuniculus (Rabbit).

CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.

NCBI\_TaxID:9986;

OK [1]

RN SEQUENCE FROM N.A.

RP STRAIN-New Zealand white; TISSUE-Skeletal muscle;

RA Maeda K., Hostinova E., Roesch-Kleinhauf A., Schuster H., Gasperik J., Wittinghofer A.;

RT "Isolation, sequencing of myosin heavy chain cDNA from rabbit skeletal muscle and a novel cosynthesis of S-1 fragment with the essential and regulatory light chains."

RL Submitted (Aug-1995) to the EMBL/GenBank/DBJ databases.

CC -!- FUNCTION: MUSCLE CONTRACTION.

CC -!- SUBUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2 HEAVY CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC) AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).

CC -!- SUBCELLULAR LOCATION: Thick filaments of the myofibrils.

CC -!- DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES, CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.

CC -!- MISCELLANEOUS: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT MEROMYOSIN (LM) AND 1 HEAVY MEROMYOSIN (HM). IT CAN LATER BE SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED SUBFRAGMENT (S2).

CC -!- SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.

CC -!- SIMILARITY: CONTAINS 1 IO DOMAIN.

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CC EMBL: U32574; AA174199.1; -

DR HSSP: P13538; 2MYS.

DR InterPro: IPR000048; IO\_region.

DR InterPro: IPR004009; Myosin\_N.

DR InterPro: IPR002928; Myosin\_tail.

DR InterPro: IPR001609; myosin\_head.

DR Pfam: PF00063; myosin\_head; 1.

DR Pfam: PF00612; IO; 2.

DR Pfam: PF01576; Myosin\_tail; 1.

DR Pfam: PF02736; Myosin\_N; 1.

DR PRINTS: PRO00193; MYOSINHEAVY.

DR ProDom: PD000355; myosin\_head; 1.

DR SMART: SM00015; IO; 1.

DR SMART: SM00242; MYSC; 1.

DR PROSITE: PS50096; IO; 1.

DR Myosin: Muscle protein; Coiled coil; Thick filament; Actin-binding; Calmodulin-binding; ATP-binding; Methylation; Alkylation; Multigene family.

KW MYOSIN HEAD-LIKE.

FT DOMAIN 1 783

FT DOMAIN 784 813

FT DOMAIN 842 1938

FT NP\_BIND 179 186

FT DOMAIN 658 680

FT DOMAIN 760 774

FT MOD\_RES 35 35

FT MOD\_RES 130 130

FT MOD\_RES 552 552

FT MOD\_RES 756 756

FT MOD\_RES 698 698

FT MOD\_RES 708 708

SO SEQUENCE 1938 AA; 223064 MW; D8A8A2EC5B182626 CRC64;

Query Match 15.3%; Score 182.5; DB 1; Length 1938;

Best Local Similarity 22.5%; Pred. No. 0.022;

Matches 81; Conservative 54; Mismatches 96; Indels 129; Gaps 13;

QY 8 VQSEEDVTAQFESYKALITNSLQEKRAAKAGKNAE-----DVHQIILATSS 63

DB 1210 IDNLRVKKLEKSELMKIIDL-----ASNMENVSAKAGLQKMGCTLEQVSELT 1265

QY 64 NOEYRMLDQTSALKETELKETT-----VSFLQKITDLOQLKQ 106

DB 1266 EEEHRLINDSAORARLQTESGERSROLDKDSIVSOLSRGKAFTQOIEBLKQLEEE 1325

QY 107 -----EED-----FRKQLEDEGRKAKENTTAELTEINKRLLY----- 142

DB 1326 IKAASALAHAIQSRHDDLLREYEEQEKAKELQGRAMSVANSEVQMRKYETDAIOR 1385

QY 143 -EELYNKTKPROIOLD-----AFVEKQALLNE-----HGAQEQQL 177

DB 1386 TEELSEAKKKLAQQLQDAEHEVAVNKKASLEKTKQRLQNEVEDLMIDVERTNAACAL 1445

QY 178 NKIRDSYAKLLG-----HONLKO-----KIKHYVK-----LKDEN 207  
 DB 1446 DKQKRFDPKILAEWKHEEYTHAELEASOKESRSLSTEFYKVNAAEESIDOLETLKREN 1505  
 QY 208 SOLKSEVSKIRCOLAR-----KKO-----SETKIOELNKVGLK 242  
 DB 1506 KNIQOEISDLTEGIAAGKRRIHELEKVKQVDEKSELQALAEAEASLEHEGKILRIQ 1565

RESULT 7  
 MYH3\_RAT  
 ID MYH3\_RAT STANDARD: PRT: 1940 AA.  
 AC P12847;  
 DT 01-OCT-1989 (Rel. 12, Created)  
 DT 01-OCT-1989 (Rel. 12, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Myosin heavy chain, fast skeletal muscle, embryonic.  
 GN MYH3.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_Taxid=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=87060988; PubMed=3783701;  
 RA Strehler E.E., Strehler-Page M.-A., Perriard J.C., Periasamy M.,  
 Nadal-Ginard B.,  
 RT "Complete nucleotide and encoded amino acid sequence of a mammalian  
 RT myosin heavy chain gene. Evidence against intron-dependent evolution  
 RT of the rod".  
 RL J. Mol. Biol. 190:291-317(1986).  
 CC -1- FUNCTION: MUSCLE CONTRACTION.  
 CC -1- SUBUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2  
 CC HEAVY CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC)  
 CC AND 2 REGULATOR LIGHT CHAIN SUBUNITS (MLC-2).  
 CC -1- SUBCELLULAR LOCATION: Thick filaments of the myofibrils.  
 CC CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES.  
 CC CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.  
 CC -1- PFM: TWO CYSTEINE RESIDUES IN THE S1 DOMAIN ARE SELECTIVELY  
 CC AKTYLATED AND ARE REQUIRED FOR MYOSIN ATPASE ACTIVITY.  
 CC -1- MISCELLANEOUS: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT  
 CC MEROMYOSIN (LM) AND 1 HEAVY MEROMYOSIN (HM). IT CAN LATER BE  
 CC SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED  
 CC SUBFRAGMENT (S2).  
 CC -1- SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 1 IQ DOMAIN.  
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 CC EMBL: X04267; CAA27817.1.  
 DR PIR: A24922; A24922.  
 DR HSSP: P13538; 2MYS.  
 DR InterPro: IPR000048; IQ\_region.  
 DR InterPro: IPR004009; Myosin\_N.  
 DR InterPro: IPR002928; Myosin\_N.  
 DR InterPro: IPR002017; Spectin.  
 DR InterPro: IPR001609; myosin\_head.  
 DR Pfam: PF00063; myosin\_head; 1.  
 DR Pfam: PF00612; IQ; 2.  
 DR Pfam: PF01576; Myosin\_tail; 1.  
 DR Pfam: PF02736; Myosin\_N; 1.  
 DR PRINTS: PR00193; MYOSINHEAVY.  
 DR PRODOM: PD000355; MYOSINHEAVY.  
 DR SMART: SM00015; IQ; 1.  
 DR SMART: SM00242; MYSC; 1.  
 DR SMART: SM00242; MYSC; 1.

DR PROSITE: PS50096; IQ; 1.  
 KW Myosin: Muscle protein, coiled coil, thick filament, actin-binding;  
 KW Calmodulin-binding; ATP-binding; Methylation; Alkylation;  
 KW Multigene family.  
 FT DOMAIN 1 781 MYOSIN HEAD-LIKE.  
 FT DOMAIN 840 811 IQ.  
 FT DOMAIN 840 1933 COILED COIL (POTENTIAL).  
 FT NP\_BIND 179 186 ATP (POTENTIAL).  
 FT DOMAIN 656 678 ACTIN-BINDING.  
 FT MOD\_RES 758 772 ACTIN-BINDING.  
 FT MOD\_RES 130 130 METHYLATION (TRI-) (POTENTIAL).  
 FT MOD\_RES 696 696 ALKYLATION (SH-1).  
 FT MOD\_RES 706 706 ALKYLATION (SH-2).  
 SQ SEQUENCE 1940 AA; 223857 MW; B50546596E5696 CRC64;

Query Match 15.2%; Score 181.5; DB 1; Length 1940;  
 Best local similarity 19.4%; Pred. No. 0.025;  
 Matches 69; Conservative 62; Mismatches 104; Indels 121; Gaps 7;

QY 8 VQSLDYTAQFESYKALTASFEIDPLKLENSLOEKAKKAKNMDVGHQILATESNOEY 67  
 DB 1208 IDNLQVAKOKLEKSEFKLEIDLSSVSASVSKSKANLEKICRTLEDQLEARGKNEET 1267  
 QY 68 VRMLDIQTSALKETBEIKET-----VSFLQKITDLOQLQOQED- 109  
 DB 1268 QRSLSLTTQKSRLOTEGELSLRLEEKESIVQSLRSQAFYQOIEELKQLEENKAK 1327  
 QY 110 FRKLEDEGRKAKKENTLELEIKMKRLYE----- 143  
 DB 1328 MALAHLOSRHDCDLREYEEQEGKALQALSKANSEVQMTKYETDAIQTEEL 1387  
 QY 144 ELYN-----KTR----- 150  
 DB 1388 EFAKKLAQRLDSEQVEAVNAKCSLEKTKRLOGEVEDLMDVERANSALAAADKKQ 1447  
 QY 151 PEOIOLAEFEVKQALLNEHGAQOELNKRIRDSYAKLLG-----HONLK 194  
 DB 1448 RNDKVLAWMKTKCESSQALEFAKESRSLSTEFKLNVAEALDQLETKREKNLE 1507  
 QY 195 QKIKHYVKLEDSOLKSEVSKIRCOLARKK-----QSETKIOELNKVGLK 242  
 DB 1508 QELADLTETGIAENGKRIHELEKSKROMELEKADIQALAEAEALAEHEBAKILRIQ 1563

RESULT 8  
 MYH2\_HUMAN  
 ID MYH2\_HUMAN STANDARD: PRT: 1941 AA.  
 AC Q9URX2; Q16229; Q14322;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Myosin heavy chain, skeletal muscle, adult 2 (Myosin heavy chain IIA)  
 DE (MYHC-IIa).  
 GN MYH2 OR MYHSA2.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 OX NCBI\_Taxid=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RP TISSUE=Skeletal muscle;  
 RC MEDLINE=99318869; PubMed=10388558;  
 RX Weiss A., Schiaffino S., Leinwand L.A.,  
 RA "Comparative sequence analysis of the complete human sarcomeric myosin  
 RT heavy chain family: implications for functional diversity".  
 RL J. Mol. Biol. 290:61-75(1999).  
 RL [2]  
 RP SEQUENCE OF 1711-1941 FROM N.A.  
 RP TISSUE=Skeletal muscle;  
 RC MEDLINE=95109625; PubMed=7545970;  
 RX Smerda V., Karsch-Mizrachi I., Campione M., Leinwand L.,  
 RA Schiaffino S.,  
 RT "Type Iix myosin heavy chain transcripts are expressed in type IIB

RT Fibers of human skeletal muscle.  
 RL Am. J. Physiol. 267:C1723-C1728(1994);  
 RN [3]  
 RP SEQUENCE OF 1823-1941 FROM N.A.  
 RC TISSUE-Skeletal muscle;  
 RX MEDLINE-95270723; PubMed-7751403;  
 RA Enlioni S., Sant'ana Pereira J., Sargeant T., Young A., Goldspink G.;  
 RT "Characterization of human skeletal muscle fibres according to the  
 RT myosin heavy chains they express."  
 RL J. Muscle Res. Cell Motil. 16:35-43(1995).  
 CC -1- FUNCTION: MUSCLE CONTRACTION.  
 CC -1- SUBUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2  
 CC HEAVY CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC).  
 CC AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).  
 CC -1- SUBCELLULAR LOCATION: Thick filaments of the myofibrils.  
 CC -1- DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING  
 CC CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES,  
 CC CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.  
 CC -1- PTM: TWO CYSTEINE RESIDUES IN THE SI DOMAIN ARE SELECTIVELY  
 CC ALKYLATED AND ARE REQUIRED FOR MYOSIN ATPASE ACTIVITY.  
 CC -1- MISCELLANEOUS: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT  
 CC MEROMYOSIN (LM) AND 1 HEAVY MEROMYOSIN (HM). IT CAN LATER BE  
 CC SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED  
 CC SUBFRAGMENT (S2).  
 CC -1- SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 1 IQ DOMAIN.  
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 CC  
 DR EMBL: AF11784; AB29950.1;  
 DR EMBL: S73840; AAC13916.1;  
 DR EMBL: Z32858; CAA83687.1;  
 DR HSSP: P13538; 2MYS.  
 DR Genew: HGNC:7572; MYH2.  
 DR MIM: 160740;  
 DR InterPro: IPR000048; IQ\_region.  
 DR InterPro: IPR004009; Myosin\_N.  
 DR InterPro: IPR002928; Myosin\_tail.  
 DR InterPro: IPR001609; myosin\_head.  
 DR Pfam: PF00063; myosin\_head.1.  
 DR Pfam: PF00612; IQ\_2.  
 DR Pfam: PF01576; Myosin\_tail.1.  
 DR Pfam: PF02736; Myosin\_N.1.  
 DR PRINTS: PR00193; MYOSINHEAVY.  
 DR ProDom: PD000355; myosin\_head.1.  
 DR SMART: SM00015; IQ\_1.  
 DR SMART: SM00242; MYSC\_1.  
 DR PROSITE: PS50096; IQ\_1.  
 DR Myosin\_Muscle\_protein; Coiled coil; Thick filament; Actin-binding;  
 KW Calmodulin-binding; ATP-binding; Methylation; Alkylation;  
 KW Multigene family;  
 FT DOMAIN 1 786 MYOSIN HEAD-LIKE.  
 FT DOMAIN 787 816 IQ.  
 FT NP\_BIND 845 1941 COILED COIL (POTENTIAL).  
 FT NP\_BIND 179 186 ATP (POTENTIAL).  
 FT CONFLICT 1844 1844 K -> R (IN REF. 3).  
 SQ SEQUENCE 1941 AA; 223043 MW; 681E866F83AEAB3F CRC64;  
 Query Match 15.1%; Score 180.5; DB 1; Length 1941;  
 Best Local Similarity 24.2%; Pred. No. 0.028;  
 Matches 87; Conservative 50; Mismatches 94; Indels 129; Gaps 15;  
 QY 8 VOSLDVTAOFESYKALTSIEDLKLENSLOEKAARKNAE----DVQHQLATSS 63  
 DB 1213 IDNIGRVOKLEKESEKMEIDLD-----ASNVEVYSKAKGKLMCKRTLEQSLSEKSK 1268.  
 QY 64 NOEYRMLD-----LQTSKSA--LKETEIKEITVS-----FLQKITDLOQLKQO 106

Db 1269 EEEQORILINDLTAQRGLQTESSEFSRQIDKEKALVSQLSRGKAFVQOIBELKROLEE 1328  
 QY 107 -----EED---FKOLEDEGRKAEKENTVTLDEIEIKMKRLY----- 142  
 Db 1329 IKAKNALAHALOSSRHCDLLREQYEDESESKAEIQLSKANTEVAVQMKRTYTDIAQR 1388  
 QY 143 -EELYNKTKEPFOIOLDA-----FEVERQALNE-----HGAQEQ 117  
 Db 1389 TEELFEKKKLAQRLOAAEEHVEVNAKCKASLEKTKORLQNEVEDMLDYERTNAACAL 1448  
 QY 178 NKIRDSYAKLLG-----HONLKO-----KIKHYK-----LKDN 207  
 Db 1449 DKQORNDKILAEWKQCEETHAELEASQKEASLSTGLPKIKNAVEESLDQLETKREN 1508  
 QY 208 SOKSEVSKRQOLAK-----KO-----SETKLOELNKVIGIK 242  
 Db 1509 KNLQELISDLTEQIAEGKRRIHELEKIKQVEQKCELAQALAEAEASLEHEEGKILRIQ 1568  
 RESULT 9  
 MYSS\_CHICK STANDARD; PRT; 1938 AA.  
 ID MYSS\_CHICK  
 AC P13538; 013228;  
 DT 01-JAN-1990 (Rel. 13, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Myosin heavy chain, skeletal muscle, adult.  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 OX NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-White leghorn; TISSUE-Pectoralis muscle;  
 RA Chao T.H., Bandman E., Moore L.;  
 RT "Cloning, nucleotide sequence and characterization of a full-length  
 RT cDNA encoding the myosin heavy chain from adult chicken pectoralis  
 RT major muscle."  
 RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE OF 1-205.  
 RC TISSUE-Pectoralis muscle;  
 RX MEDLINE-92041767; PubMed-1939027;  
 RA Hayashida M., Maeta T., Matsuda G.;  
 RT "The primary structure of skeletal muscle myosin heavy chain: I.  
 RT Sequence of the amino-terminal 23 kDa fragment."  
 RL J. Biochem. 110:54-59(1991).  
 RN [3]  
 RP SEQUENCE OF 206-636.  
 RC TISSUE-Pectoralis muscle;  
 RX MEDLINE-92041768; PubMed-1939028;  
 RA Komine Y., Maeta T., Matsuda G.;  
 RT "The primary structure of skeletal muscle myosin heavy chain: II.  
 RT Sequence of the 50 kDa fragment of subfragment-1."  
 RL J. Biochem. 110:60-67(1991).  
 RN [4]  
 RP SEQUENCE OF 637-837.  
 RC TISSUE-Pectoralis muscle;  
 RX MEDLINE-92041769; PubMed-1939029;  
 RA Maeta T., Miyaniishi T., Matsuzono K., Tanioka Y., Matsuda G.;  
 RT "The primary structure of skeletal muscle myosin heavy chain: III.  
 RT Sequence of the 22 kDa fragment and the alignment of the 23 kDa, 50  
 RT kDa, and 22 kDa fragments."  
 RL J. Biochem. 110:68-74(1991).  
 RN [5]  
 RP SEQUENCE OF 838-1938.  
 RC TISSUE-Pectoralis muscle;  
 RX MEDLINE-92041770; PubMed-1939030;  
 RA Maeta T., Yajima E., Nagata S., Miyaniishi T., Nakayama S., Matsuda G.;  
 RT "The primary structure of skeletal muscle myosin heavy chain: IV.  
 RT Sequence of the rod, and the complete 1,938-residue sequence of the

RT heavy chain.";  
 RN J. Biochem. 110:75-87(1991).  
 [6]  
 RP PRELIMINARY SEQUENCE OF 1-808  
 RX MEDLINE=87092420; PubMed=3467365;  
 RA Maita T., Hayashida M., Tanioka Y., Komine Y., Matsuda G.,  
 RT "The primary structure of the myosin head";  
 RL Proc. Natl. Acad. Sci. U.S.A. 84:416-420(1987).  
 RN [17]  
 RP SEQUENCE OF 842-1270.  
 RX MEDLINE=90121764; PubMed=2610940;  
 RA Watanabe B.;  
 RT "Complete amino-acid sequence of subfragment-2 in adult chicken  
 RL Biol. Chem. Hoppe-Seyler 370:1027-1034(1989).  
 RN [18]  
 RP SEQUENCE OF 852-1108.  
 RX MEDLINE=89374803; PubMed=2775482;  
 RA Watanabe B.;  
 RT "Amino-acid sequence of the short subfragment-2 in adult chicken  
 RL Biol. Chem. Hoppe-Seyler 370:549-558(1989).  
 RN [19]  
 RP SEQUENCE OF 1145-1270.  
 RX MEDLINE=89228549; PubMed=2713098;  
 RA Watanabe B.;  
 RT "Amino-acid sequence of the hinge region in chicken myosin  
 RL Biol. Chem. Hoppe-Seyler 370:55-61(1989).  
 RN [10]  
 RP SEQUENCE OF 1857-1938 FROM N.A.  
 RX MEDLINE=87217964; PubMed=3034534;  
 RA Moriarty D.M., Barringer K.J., Dodgson J.B., Richter H.E.,  
 RT "Young R.B.;  
 RL "Genomic clones encoding chicken myosin heavy-chain genes";  
 RN DNA 6:91-99(1987).  
 RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 1-843.  
 RX MEDLINE=93303624; PubMed=8316857;  
 RA Rayment I., Rypniewski W.R., Schmidt-Base K., Smith R.,  
 RA Tomchick D.R., Bennett M.W., Winkelmann D.A., Wesenberg G.,  
 RT "Three-dimensional structure of myosin subfragment-1: a molecular  
 RL motor";  
 RN Science 261:50-58(1993).  
 RT -1- FUNCTION: MUSCLE CONTRACTION. MYOSIN IS A PROTEIN THAT BINDS TO  
 CC -1- SUBUNIT. MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2  
 CC HEAVY CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC)  
 CC AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).  
 CC -1- SUBCELLULAR LOCATION: Thick filaments of the myofibrils.  
 CC -1- DOMAIN: THE ROD-LIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING  
 CC CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.  
 CC -1- PTM: TWO CYSTEINE RESIDUES IN THE S1 DOMAIN ARE SELECTIVELY  
 CC ALKYLATED AND ARE REQUIRED FOR MYOSIN ATPASE ACTIVITY.  
 CC MISCELLANEOUS: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT  
 CC MEROMYOSIN (LM) AND 1 HEAVY MEROMYOSIN (HM). IT CAN LATER BE  
 CC SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED  
 CC SUBFRAGMENT (S2).  
 CC -1- SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 1 IQ DOMAIN.  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 DR EMBL; U07231; AAB47555.1;  
 DR EMBL; M16557; AAA48970.1;

DR PIR: PX0050; PX0051.  
 DR PIR: A26821; A26821.  
 DR PIR: S02082; S02082.  
 DR PIR: S04501; S04501.  
 DR PIR: S05515; S05515.  
 DR PDB: 2MTS; 1J-JAN-97.  
 DR InterPro: IPR000048; IQ\_region.  
 DR InterPro: IPR004009; Myosin\_N.  
 DR InterPro: IPR002928; Myosin\_tail.  
 DR InterPro: IPR001609; myosin\_head.  
 DR Pfam: PF00063; myosin\_head.  
 DR Pfam: PF00612; IQ: 2.  
 DR Pfam: PF01576; Myosin\_tail; 1.  
 DR Pfam: PF02736; Myosin\_N; 1.  
 DR ProDom: PD000355; myosin\_head; 1.  
 DR SMART; SM00015; IQ; 1.  
 DR SMART; SM00242; MYSC; 1.  
 DR ProSite; PS50096; IQ; 1.  
 DR Myosin: Muscle protein. Coiled coil; Thick filament; Actin-binding;  
 KW ATP-binding; Methylation; Alkylation; Phosphorylation; Acetylation;  
 KW Calmodulin-binding; Multigene family; 3D-structure.  
 FT INIT\_MET 0  
 FT DOMAIN 1 782  
 FT 783 812  
 FT 838 840  
 FT 841 1938  
 FT NP\_BIND 179 186  
 FT 657 679  
 FT 759 773  
 FT MOD\_RES 1 1  
 FT MOD\_RES 35 35  
 FT MOD\_RES 130 130  
 FT MOD\_RES 551 551  
 FT MOD\_RES 755 755  
 FT MOD\_RES 697 697  
 FT MOD\_RES 707 707  
 FT CONFLICT 907 907  
 FT CONFLICT 980 980  
 FT CONFLICT 1343 1343  
 FT CONFLICT 1545 1545  
 FT CONFLICT 1796 1797  
 FT CONFLICT 1830 1830  
 FT CONFLICT 1863 1863  
 FT CONFLICT 1929 1931  
 SQ SEQUENCE 1938 AA; 223013 MW; EDDD1GCA2681E10F CRC64;  
 Query Match 15.0%; Score 179.5; DB 1; Length 1938;  
 Best Local Similarity 20.5%; Pred. No. 0.032;  
 Matches 73; Conservative 55; Mismatches 107; Indels 121; Gaps 9;  
 OY 8 VQSLDYTAQFEESKALTASIEDLKENSLOEKAKAGNAEDVOHILATSSNOEY 67  
 DB 1209 IDNLRVKQKLEKSKSLKNEIDLASNMESVSKANLEKMCRTLEDISEIKTEEON 1268  
 OY 68 VRMLDQTSALKETEI-----KETTVS-----FLQITDLONLKOE 107  
 DB 1269 QRMNDLNTQRLQGLTGETYSQDAEKDALISQLSRGQSGFTQGLLEKRLHEETAK 1328  
 OY 108 -----EPRKQLEDEGRKAEKETTALTEELINKRRLY-----EEL 145  
 DB 1329 MALAHLAGARHDCCLLRQYEEOAKGELORALSKANSEVAQWRTEYEDALQRTTEL 1388  
 OY 146 YNKTQFOQLD-----AFEEVQALINE-----HGAAGQELNKR 181  
 DB 1389 EERKKKLAQRLQDAEHEEVAANAKASLEKTRQRLQNEVEDLMDVENSNAACALDKQ 1448  
 OY 182 DSYAKILGHQNLK-----OKIHVYKLKDNLSQK 211  
 DB 1449 KNEFDILAEKQKYEETOTELASOKESRSLSLETFKKNAYEESLDHLFTLKREKNLQ 1508  
 OY 212 SEVSKLRQOLA-----RK-----KQSEPTLOELNKKVIGIK 242  
 DB 1509 QEIDLTLQIAEGGKAVAELEKVKKHVQEKSELOASLEAEKSLHEEKGKILRLQ 1564



```

SQ      SEQUENCE     1939 AA;  223012 MW;  40BLADLD77AA7DE CRC64;
Query Match          15.0%; Score 179.5; DB 1; Length 1939;
Best Local Similarity 18.7%; Pred. No. 0.032;
Matches    67; Conservative   61; Mismatches 104; Indels 127; Gaps 7;

OY      VOSLEDVAQOEESVKALPASFIEDPKLENSLSJOEKAAGKNAEDVQHILATESNOEY 67
       :|::||::||::||::||::||::||::||::||::||::||::||::||::||
DB      1211 IDSLORVQOKLEKEKSELKMEINDLASMETVSRAKANFEKMCRTLEDQLSEIKTEEEQ 1270
       68 VRMLIDLOTKALKETEIKEIT-----VSFLQRITDLOLQKOQEED- 109
OY      1271 QRLNELSAQARLHTSEGFSRDLDEDAVSOLSRKQAFPOQIEELKROLEEETKAK 1330
       110 -----FRKODEEGRRKAEKENTTALETJEBINKRWLYE----- 143
DB      1331 STLHAQAASAHDDDLLREQYEPEEQEAQAEILOGRGSKANSEVAQMRTKYETDALQRTIEL 1390
       110 ::||::||::||::||::||::||::||::||::||::||::||::||
OY      144 -----ELYNTKPPQIOL----- 156
DB      1391 EEANKKLQRLQDAEEHVEAVNSCASLEKTROPLONEVEDLMIDVERSNACIALDKQ 1450
OY      157 -----DAFEVEKQALLNENGAQOELNKIRDSYATLLGH-----QNLK 194
DB      1451 RNFDKVLAEMKQKYTEQALEAQSCKERSRSSTELPFKKNAYESLHLLETLRKENNNLQ 1510
OY      195 OKI-----KHVVKLKDENSOLKSEVSKLRCLOLAKKQOSEFKLOEELNVGLGK 242
       ||::||::||::||::||::||::||::||::||::||::||::||::||
DB      1511 QEISDLFQIAEGGHHHELEKVKKOLDHEKSELQTSL---EADVASLHEHGKILRIQ 1566

RESULT 11
MFP1_LYCES
ID      MFP1_LYCES      STANDARD;      PTR;      697 AA.
AC      P93203;
DT      16-OCT-2001 (Rel. 40, Created)
DT      16-OCT-2001 (Rel. 40, Last sequence update)
DT      16-OCT-2001 (Rel. 40, Last annotation update)
DE      MAR binding filament-like protein 1.
GN      MFP1.
OS      Lycopersicon esculentum (Tomato).
OC      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC      Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC      Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
OX      NCBI_TaxID=4081;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=cv. VENT Cherry; TISSUE=Fruit;
RX      MEDLINE=971112038; PubMed=8953774;
RA      Meier I., Phelan T., Gruijssem W., Spiker S., Schneider D.;
RT      "MFP1, a novel plant filament-like protein with affinity for matrix
RL      attachment region DNA.";
RL      Plant Cell 8:2105-2115(1996).
CC      -1- FUNCTION: BINDS DNA. INTERACTS WITH CHROMATIN VIA MATRIX
CC      ATTACHMENT REGIONS (MARS). LIKELY TO PARTICIPATE IN NUCLEAR
CC      ARCHITECTURE BY CONNECTING CHROMATIN WITH THE NUCLEAR MATRIX AND
CC      POTENTIALLY WITH THE NUCLEAR ENVELOPE.
CC      -1- SUBCELLULAR LOCATION: NUCLEAR MATRIX.
CC      -----
CC      CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL Outstation at
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use by non-profit institutions as long as its content is in no way
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CC      entities requires a licenseesib.ch) (See http://www.isb-sib.ch/announce/
CC      or send an email to licensesib-sib.ch).
DR      EMBL; Y07861; CAA69181.1; -
KW      Nuclear protein; DNA-binding; Coiled coil.
FT      DOMAIN              125      681      COILED COIL (POTENTIAL).
FT      DOMAIN              10      15      POLY-SER.
SQ      SEQUENCE     697 AA;  700A566D8D6A7E49 CRC64;

```

Query Match 15.0%; Score 179; DB 1; Length 697;  
 Best Local Similarity 25.6%; Pred. No. 0.012;  
 Matches 72; Conservative 57; Mismatches 96; Indels 56; Gaps 12.

QY 1 QEKDSWQSLQEDVTAQESKALTAS---EIEDIKLENSLSQEKAKAGNAEDVQH--55  
 DB 427 QESLENSRSEVSDITVQLEQRLDSKLEKREVSQLOME---LEEFRASTQNRIDETKISS 483  
 QY 56 QILADE-----SSNOEYVRMLDQTSALKETIKITVYSFLQKITDLONLQKQ 106  
 DB 484 ELALAEITTTKELLKKTNEEHNTMSDELAVASENDSLOTEL-VNAYKREHTRNELKOE 542  
 QY 107 -----EEDFRKQLEDEGRKAKEENTAEITEINRWL-LVEEL 145  
 DB 543 KTVITTELEELKFLQSTTRKEKRLKSLDE---LEE---ATSLDEINNVALLAEEL 595  
 QY 146 YNKTQPPQIQLADEVEKQALLNHEGAQOLNKRIPDSYAKL-----GHOMIKOKIKHYV 201  
 DB 596 ELATSRNSLSEDEREVRHQSSEKQISQEAQENLEDAHSIVMLGKERESLEKRAK---652  
 QY 202 KLEPENSQKSEVSKLRQCLAKKQSEETKLOEELNKVLGTR 242  
 DB 653 KLEDEMAAKGEILRLKSQINSVK---APVEDEKVVAGEK 690.

RESULT 12  
 MYH1\_HUMAN STANDARD; PRT; 1939 AA.  
 ID MYH1\_HUMAN  
 AC P12882; Q9Y622;  
 DT 01-OCT-1989 (Rel. 12, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Myosin heavy chain, skeletal muscle, adult 1 (Myosin heavy chain  
 Iix/d) (MyHC-Iix/d).  
 GN MYH1.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_Taxid=9606;  
 RN 11  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Skeletal muscle;  
 RA MEDLINE=99318659; PubMed=10388558;  
 RA Weiss A., Schiaffino S., Lelwand L.A.;  
 RT "Comparative sequence analysis of the complete human sarcomeric myosin  
 heavy chain family: implications for functional diversity.";  
 RL J. Mol. Biol. 290:61-75(1999).  
 RN [2]  
 RP SEQUENCE OF 1064-1939 FROM N.A.  
 RX MEDLINE=66176778; PubMed=2421254;  
 RA Saez L., Lelwand L.A.;  
 RT "Characterization of diverse forms of myosin heavy chain expressed in  
 adult human skeletal muscle.";  
 RL Nucleic Acids Res. 14:2951-2969(1986).  
 CC 1- FUNCTION: MUSCLE CONTRACTION.  
 CC 1- SUBUNIT: MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2  
 HEAVY CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC)  
 AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).  
 CC 1- SUBCELLULAR LOCATION: Thick filaments of the myofibrils.  
 CC 1- DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING  
 CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES,  
 CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.  
 CC 1- PTM: TWO CYSTEINE RESIDUES IN THE SI DOMAIN ARE SELECTIVELY  
 ALKYLATED AND ARE REQUIRED FOR MYOSIN ATPASE ACTIVITY.  
 CC 1- MISCELLANEOUS: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT  
 MEROMYOSIN (LMH) AND 1 HEAVY MEROMYOSIN (HMH). IT CAN LATER BE  
 SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED  
 SUBFRAGMENT (S2).  
 CC 1- SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.  
 CC 1- SIMILARITY: CONTAINS 1 IO DOMAIN.  
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CC EMBL; AF111785; AAD29951.1;  
 DR EMBL; X03740; CAA27380.1;  
 DR PIR; A23767; A23767.  
 DR HSSP; P13538; 2MYS.  
 DR Genew; HGNC:7567; MYH1.  
 DR MIM: 160730;  
 DR InterPro; IPR000048; IO\_region.  
 DR InterPro; IPR004009; Myosin\_N.  
 DR InterPro; IPR002928; Myosin\_tail.  
 DR InterPro; IPR001609; myosin\_head.  
 DR Pfam; PF00063; myosin\_head\_1.  
 DR Pfam; PF00612; IO\_2.  
 DR Pfam; PF01576; Myosin\_tail\_1.  
 DR Pfam; PF02736; Myosin\_N\_1.  
 DR PRINTS; PR00193; MYOSINHEAVY.  
 DR ProDom; PD000355; myosin\_head\_1.  
 DR SMART; SM00015; IO\_1.  
 DR SMART; SM00242; MYSC\_1.  
 DR PROSITE; PS50096; IO\_1.  
 KW Myosin; Muscle protein; Coiled coil; Thick filament; Actin-binding;  
 KW Calmodulin-binding; ATP-binding; Methylation; Alkylation;  
 KW Multigene family.  
 FT DOMAIN 1 784  
 FT MYOSIN HEAD-LIKE.  
 FT COILED COIL (POTENTIAL).  
 FT ATP (POTENTIAL).  
 FT ACTIN-BINDING (BY SIMILARITY).  
 FT ACTIN-BINDING (BY SIMILARITY).  
 FT METHYLATION (TR-1) (POTENTIAL).  
 FT ALKYLATION (SH-1) (POTENTIAL).  
 FT ALKYLATION (SH-2) (POTENTIAL).  
 FT MOD\_RES 699 699  
 FT MOD\_RES 709 709  
 FT CONFICT 1131 1131  
 FT CONFICT 1139 1139  
 FT CONFICT 1158 1158  
 FT CONFICT 1163 1163  
 FT CONFICT 1286 1289  
 FT CONFICT 1302 1303  
 FT CONFICT 1451 1451  
 FT CONFICT 1470 1470  
 FT CONFICT 1473 1474  
 FT CONFICT 1569 1569  
 FT CONFICT 1598 1598  
 FT CONFICT 1606 1606  
 FT CONFICT 1643 1643  
 FT CONFICT 1648 1648  
 FT CONFICT 1750 1750  
 FT CONFICT 1822 1822  
 FT CONFICT 1845 1845  
 SO SEQUENCE 1939 AA; 223114 MW; 39AD26AB790FA53 CRC64;

Query Match 14.9%; Score 178.5; DB 1; Length 1939;  
 Best Local Similarity 23.3%; Pred. No. 0.036;  
 Matches 84; Conservative 51; Mismatches 96; Indels 129; Gaps 14.

QY 8 VQSLQEDVTAQESKALTAS---EIEDIKLENSLSQEKAKAGNAED---VQHQILATSS 63  
 DB 1211 IDNLRVQKQLEKESSEKMEITDL---ASNMETVSKAGMLKRCALQLEQLSEIKTK 1266  
 QY 64 NOEYRMLDQTSALKETI-----KEIVYS-----FLOKITDLONLQKQ 106  
 DB 1267 EEEQRLINDLAQARALQTESGEYSRQLEKQDTVLSQSRKQAFQOIEELKQLESE 1326  
 QY 107 -----EED---FKQIODEGRKAKEENTAEITEINRWL-----142  
 DB 1327 IKAQSALAHALQSSRHDDQLREQYEEQDEAAELQRMASKNSEVAQWRTYETDAJOR 1386  
 QY 143 -EELYNKTRKPPQIQLD-----AFVEKQALLNE-----HGAAGQSL 177

Db 1387 TEELEKAKKLAORLQDAEHEVAANAKASLEKTKORLONEVEDIMIDVERTNAACAL 1446  
 QY 178 NKTRDSYAKLLG-----HONLKO-----KIRHVYK-----LKJDN 207  
 Db 1447 DKQORNDKTLAEWKQKCEETHAELEASOKESLSLEFKIKYNAEESLDQJLETKREN 1506  
 QY 208 SOLKSEVSKIRCOLAR-----KKO-----SETKLOEELNKVGLIK 242  
 Db 1507 KNQOETISDLTEQIAEGGKRIHLEKIKKQVEDEKSELQALAEAEASLEHEGKILIRIQ 1566  
 RESULT 13  
 MYH3\_HUMAN STANDARD; PRT; 1940 AA.  
 ID MYH3\_HUMAN  
 AC P11055; Q15492;  
 DT 01-JUL-1989 (Rel. 11, Created)  
 DT 01-JUL-1989 (Rel. 11, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Myosin heavy chain, fast skeletal muscle, embryonic (Muscle embryonic  
 myosin heavy chain) (SMCE).  
 GN MYH3.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE-89263803; PubMed-2726495;  
 RA Eller M.S., Steadman H.H., Sylvester J.E., Fertels S.H., Wu Q.-L.,  
 Rubinstein N.A., Kelly A.M., Sarkar S.;  
 RT "Nucleotide sequence of full length human embryonic myosin heavy  
 chain cDNA.";  
 RT Nucleic Acids Res. 17:3591-3592(1989).  
 RN [2]  
 RP SEQUENCE OF 774-1940 FROM N.A.  
 RA MEDLINE-90033298; PubMed-2806546;  
 RA Eller M.S., Steadman H.H., Sylvester J.E., Fertels S.H., Wu Q.-L.,  
 Raychowdhury M.K., Rubinstein N.A., Kelly A.M., Sarkar S.;  
 RT "Human embryonic myosin heavy chain cDNA. Interspecies sequence  
 conservation of the myosin rod, chromosomal locus and isoform  
 specific transcription of the gene.";  
 RT FEBS Lett. 256:21-28(1989).  
 RN [3]  
 RP SEQUENCE OF 856-1940 FROM N.A.  
 RC TISSUE-Skeletal muscle;  
 RA MEDLINE-90235862; PubMed-1691980;  
 RA Bober E., Buchberger-Seidl A., Braun T., Singh S., Goedde H.W.,  
 Arnold H.H.;  
 RT "Identification of three developmentally controlled isoforms of human  
 myosin heavy chains.";  
 RT Eur. J. Biochem. 189:55-65(1990).  
 RN [4]  
 RP SEQUENCE OF 856-1940 FROM N.A.  
 RA MEDLINE-89366648; PubMed-2771643;  
 RA Karsch-Mizrachi I., Travis M., Bleu H., Leitwand L.A.;  
 RT "Expression and DNA sequence analysis of a human embryonic skeletal  
 muscle myosin heavy chain gene.";  
 RT Nucleic Acids Res. 17:6167-6179(1989).  
 CC -1- FUNCTION: MUSCLE CONTRACTION.  
 CC -1- SUBUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2  
 HEAVY CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC)  
 AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).  
 CC -1- SUBCELLULAR LOCATION: Thick filaments of the myofibrils.  
 CC -1- DEVELOPMENTAL STAGE: ABUNDANTLY PRESENT IN FETAL SKELETAL MUSCLE  
 AND NOT PRESENT OR BARELY DETECTABLE IN HEART AND ADULT SKELETAL  
 MUSCLE.  
 CC -1- DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING  
 CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES,  
 CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.  
 CC -1- PTM: TWO CYSTEINE RESIDUES IN THE S1 DOMAIN ARE SELECTIVELY  
 AKTYLATED AND ARE REQUIRED FOR MYOSIN ATPASE ACTIVITY.  
 CC -1- MISCELLANEOUS: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT

CC MEROMYOSIN (LMN) AND 1 HEAVY MEROMYOSIN (HMN). IT CAN LATER BE  
 CC SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED  
 CC SUBFRAGMENT (S2).  
 CC -1- SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 1 IQ DOMAIN.  
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 CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
 CC  
 CC EMBL: X13988; CA32167.1;  
 CC EMBL: X13100; CA31492.1;  
 CC EMBL: X51593; CA35942.1;  
 CC EMBL: X15696; CA33731.1;  
 CC PIR: S04090; S04090.  
 CC HSP: P13538; 2MYS.  
 CC Genew: HGNC:7573; MYH3.  
 CC MIM: 160720;  
 CC InterPro: IPR000048; IQ\_region.  
 CC InterPro: IPR004009; Myosin\_N.  
 CC InterPro: IPR002928; Myosin\_tail.  
 CC InterPro: IPR001609; myosin\_head.  
 CC Pfam: PF00063; myosin\_head; 1.  
 CC Pfam: PF00612; IQ; 2.  
 CC Pfam: PF01576; Myosin\_tail; 1.  
 CC Pfam: PF02736; Myosin\_N; 1.  
 CC PRINTS: PR00193; MYOSINHEAVY.  
 CC ProDom: PD000355; myosin\_head; 1.  
 CC SMART: SM00015; IQ; 1.  
 CC SMART: SM00242; MYSC; 1.  
 CC PROSITE: PS50096; IQ; 1.  
 CC Myosin; Muscle protein; Coiled coil; Thick filament; Actin-binding;  
 CC Calmodulin-binding; ATP-binding; Methylation; Alkylation;  
 CC Multigene family.  
 CC  
 CC FT DOMAIN 1 781 MYOSIN HEAD-LIKE.  
 CC FT DOMAIN 840 811 IQ.  
 CC FT NP\_BIND 179 186 COILED COIL (POTENTIAL).  
 CC FT DOMAIN 656 678 ATP (POTENTIAL).  
 CC FT DOMAIN 758 772 ACTIN-BINDING.  
 CC FT MOD\_RES 130 130 METHYLATION (TR1-) (POTENTIAL).  
 CC FT MOD\_RES 696 696 ALKYLATION (SH-1).  
 CC FT MOD\_RES 706 706 ALKYLATION (SH-2).  
 CC FT CONFLICT 1331 1331 A -> G (IN REF. 3).  
 CC FT CONFLICT 1391 1392 KK -> OE (IN REF. 1 AND 2).  
 CC FT CONFLICT 1608 1609 SR -> RA (IN REF. 3).  
 CC FT CONFLICT 1663 1664 RG -> QT (IN REF. 2).  
 CC FT  
 CC SQ SEQUENCE 1940 AA; 224035 MW; 43CA58C6A4BA1253 CRC64;  
 CC  
 CC Query Match 14.9%; Score 178.5; DB 1; Length 1940;  
 CC Best Local Similarity 19.1%; Pred. No. 0.036;  
 CC Matches 68; Conservative 62; Mismatches 105; Indels 121; Gaps 7;  
 CC  
 CC QY 8 VQSLDYTAQFESYATATSEIEDLKLNSIQEKAARKGAEDVQHOIATNESSQY 67  
 Db 1208 IDNLQVAKQLEKRESEFKLEIDLSSMSVSKANLEKICRPLEDLSBARKNEBI 1267  
 QY 68 VMLDLQTSKALKEIKET-----VSFLQKITDQNLQKQOED- 109  
 Db 1268 QRSLSLTQKSRLOTEGELSRQLEKESIVQSRSKQATQOOTEELKROLEENNAK 1327  
 QY 110 -----FKQLEDEGRKAKEKNTAETLETKRWRLYE- 143  
 Db 1328 NALAHALQSRHDCOLLAEQVEEGRKAELQALSKANSEVAQKRTYETAIOETEL 1387  
 QY 144 -----ELYN-----KTK----- 150  
 Db 1388 EAAKKKLAORLQDSEQVEAVNAKASLEKTKORLQGEVEDLMVVERANSIAALDKKO 1447

OY 151 -----PROIOLDAFEVEKQALLNENHGAOEOJLNKIDSVAKLLG-----HONIK 194  
 DB 1448 RNDKVLAEKTKCESSQAELESLKESRSLSTELKLNKNAVEALDOLETYREKNIE 1507  
 OY 195 OKIRHVYKLDENSQKSEVSKLRQOLAKK-----QSEKLOEELNKVYLGK 242  
 DB 1508 QETADLTQIAENGKTHIELEKSKOIELEKADIOALDEAEALAEHEKATLRIO 1563

## RESULT 14

SCPL\_MESAU STANDARD: PRT: 845 AA.  
 ID SCPL\_MESAU 060563;  
 AC 060563;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Synaptonemal complex protein 1 (SCP-1 protein) (Meiotic chromosome synaptonemal complex) (Fragment).  
 GN SCPL OR SYN1.  
 OS Mesocricetus auratus (Golden hamster).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae; Mesocricetus.  
 OX NCBI\_Taxid=10036;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-Testis;  
 RX MEDLINE=95181577; PubMed=7876143;  
 RA Dobson M.J., Pearlman R.E., Karatskakis A., Spyropoulos B., Moens P.B.;  
 RT "Synaptonemal complex proteins: occurrence, epitope mapping and chromosome disjunction.";  
 RL J. Cell Sci. 107:2749-2760(1994)  
 CC -1- FUNCTION: MAJOR COMPONENT OF THE TRANSVERSE FILAMENTS OF SYNAPTONEMAL COMPLEXES (SCS), FORMED BETWEEN HOMOLOGOUS CHROMOSOMES DURING MEIOTIC PROPHASE (BY SIMILARITY). HAS NON-SPECIFIC DNA BINDING CAPABILITY.  
 CC -1- SUBCELLULAR LOCATION: NUCLEAR. IN TRIPARTITE SEGMENTS OF SYNAPTONEMAL COMPLEXES, BETWEEN LATERAL ELEMENTS IN THE NUCLEUS. FOUND ONLY WHERE THE CHROMOSOME CORES ARE SYNAPSED. ITS N-TERMINUS IS FOUND TOWARDS THE CENTRE OF THE SYNAPTONEMAL COMPLEX WHILE THE C-TERMINUS EXTENDS WELL INTO THE LATERAL DOMAIN OF THE SYNAPTONEMAL COMPLEX.  
 CC -1- DOMAIN: CONSISTS OF AN ALPHA-HELICAL STRETCH OF 700 AA RESIDUES, FLANKED BY N- AND C-TERMINAL GLOBULAR DOMAINS. THE C-TERMINAL DOMAIN HAS DNA-BINDING CAPACITY (BY SIMILARITY).  
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 CC EMBL; I32978; AAC2039.1;  
 DR Nucleic protein; Melosis; Cell division; Phosphorylation;  
 KW DNA-binding; Coiled coil.  
 FT NON-TER 1  
 FT DOMAIN <1 672 COILED COIL (POTENTIAL).  
 FT DOMAIN 553 556 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).  
 FT DOMAIN 753 756 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).  
 FT DOMAIN 830 838 ARG/LYS-RICH (BASIC).  
 SQ SEQUENCE 845 AA; 99401 MW; DFE28873C824C6A8 CnC64;

Query Match 14.8%; Score 176.5; DB 1; Length 845;  
 Best Local Similarity 23.1%; Pred. NO. 0.02;  
 Matches 79; Conservative 55; Mismatches 97; Indels 111; Gaps 14;

OY 5 DSMVOSLEDVYAOESYKALATASEIEDLKENSLO-EKAK--AGNAE-----51  
 DB 273 DEMTKFFNNNEVKLEELKTLIA---EDOKLDEKKOYKELAEELQGEQETLLLOTRK 329

OY 52 -----DVQHOIATNESSNOEYVRLDLQTRKSAKTEIR--ETVS-----FLOKI 96  
 DB 330 EVDHLEEOILVYTKISDQNSKQVEELKTR--LEEKLNAAELTACGSLSENNKLTQET 387  
 OY 97 TDLOLQOL-----KQOEEDFRKQLEDEGR-----120  
 DB 368 NDMALELKQYODITNSKQOEERMLKQIENLEEKETHLRDELESYKKEFIQOGNEVCKL 447  
 OY 121 -----KAEK-----ENTAEETLEIRKRLLYEELYNKTRFQ-----153  
 DB 448 DKSEENARSICEVYLKKEKQKILKCNKNLRKAENKSKYIEELHODENKALKKSSAES 507  
 OY 154 IQLAEFEVEKQALLNENHGAOEOJLNKIDST-----AKLGHQMLKOKIRHVYKLDENS 208  
 DB 508 KQLNAVETKVKLDLELESASAKQOEEMTDNYQKEIEVKKISEEKILGEVEKAKMVDVAV 567  
 OY 209 QLKSEVSKLRQO-----LARKKQSEFKLOELNKVYGI 241  
 DB 568 KLRKEID-LRQGHKIAEMVAMEKHKHOYDKIYVEERSEJGL 608

## RESULT 15

MYH8\_HUMAN STANDARD: PRT: 1937 AA.  
 ID MYH8\_HUMAN  
 AC P13535; Q14910;  
 DT 01-JAN-1990 (Rel. 13, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Myosin heavy chain, skeletal muscle, perinatal (MyHC-perinatal).  
 GN MYH8.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 OX NCBI\_Taxid=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-Skeletal muscle;  
 RX MEDLINE=90323631; PubMed=2373371;  
 RA Karsch-Mizrachi I., Peghali R., Shows T.B. Jr., Leinwand L.A.;  
 RT "Generation of a full-length human perinatal myosin heavy-chain-encoding cDNA.";  
 RL Gene 89:289-294(1990).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-Skeletal muscle;  
 RX MEDLINE=95324556; PubMed=7601129;  
 RA Julian E.H., Kelly A.M., Pompidou A.J., Hoffman R., Schiaffino S., Stegman H.H., Rubinstein N.A.;  
 RT "Characterization of a human perinatal myosin heavy-chain transcript.";  
 RL Eur. J. Biochem. 230:1001-1006(1995).  
 RN [3]  
 RP SEQUENCE OF 502-1937 FROM N.A.  
 RC TISSUE-Skeletal muscle;  
 RX MEDLINE=90235862; PubMed=1691980;  
 RA Robert E., Buchberger-Seidl A., Braun T., Singh S., Goede H.W., Arnold H.H.;  
 RT "Identification of three developmentally controlled isoforms of human myosin heavy chains.";  
 RL Eur. J. Biochem. 189:55-65(1990).  
 RN [4]  
 RP SEQUENCE OF 860-1937 FROM N.A.  
 RX MEDLINE=89234168; PubMed=2715179;  
 RA Peghali R., Leinwand L.A.;  
 RT "Molecular genetic characterization of a developmentally regulated human perinatal myosin heavy chain.";  
 RL J. Cell Biol. 108:1791-1797(1989).  
 RN [5]  
 RP SEQUENCE OF 1-46 FROM N.A.  
 RA Esser K., Tidhar A., Myszkowski M.;  
 RT "Isolation and characterization of the human perinatal MHC promoter.";  
 RL Submitted (MAY-1998) to the EMBL/Genbank/DBD databases.  
 CC -1- FUNCTION: MUSCLE CONTRACTION.

CC -1- SUBUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2  
CC HEAVY CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC)  
CC AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).  
CC -1- SUBCELLULAR LOCATION: Thick filaments of the myofibrils.  
CC -1- DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING  
CC CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES,  
CC CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.  
CC -1- PTM: TWO CYSTEINE RESIDUES IN THE S1 DOMAIN ARE SELECTIVELY  
CC ALKYLATED AND ARE REQUIRED FOR MYOSIN ATPASE ACTIVITY.  
CC MISCELLANEOUS: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT  
CC MEROMYOSIN (LM) AND 1 HEAVY MEROMYOSIN (HM). IT CAN LATER BE  
CC SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED  
CC SUBFRAGMENT (S2).  
CC -1- SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.  
CC -1- SIMILARITY: CONTAINS 1 IO DOMAIN.  
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DR EMBL: M36769; AAC17185.1; -  
DR EMBL: Z38133; CAA86293.1; -  
DR EMBL: X51592; CAA35941.1; -  
DR EMBL: AF067143; AAC21557.1; -  
DR PIR: A30220; A30220.  
DR HSSP: P13538; 2MTS.  
DR GeneW: HGNC:7578; MYH8.  
DR MIM: 160741; -  
DR InterPro: IPR000048; IO\_region.  
DR InterPro: IPR004009; Myosin\_N.  
DR InterPro: IPR002928; Myosin\_tail.  
DR InterPro: IPR001609; myosin\_head.  
DR Pfam: PF00063; myosin\_head; 1.  
DR Pfam: PF0612; IO; 1.  
DR Pfam: PF01576; Myosin\_tail; 1.  
DR Pfam: PF02736; Myosin\_N; 1.  
DR PRINTS: PRO0193; MYOSINHEAVY.  
DR ProDom: PD000355; myosin\_head; 1.  
DR SMART: SM00015; IO; 1.  
DR SMART: SM00242; MYSC; 1.  
DR PROSITE: PS50096; IO; 1.  
DR Myosin: Muscle protein; Coiled coil; Thick filament; Actin-binding;  
KW ATP-binding; Methylation; Alkylation; Multigene family;  
KW Calmodulin-binding.  
FT DOMAIN 1 780 MYOSIN HEAD-LIKE.  
FT DOMAIN 1 780 IO.  
FT DOMAIN 842 1937 COILED COIL (POTENTIAL).  
FT NP\_BIND 181 188 ATP.  
FT DOMAIN 658 680 ACTIN-BINDING.  
FT DOMAIN 760 774 ACTIN-BINDING.  
FT MOD\_RES 132 132 METHYLATION (TR1-) (POTENTIAL).  
FT MOD\_RES 698 698 METHYLATION (SH-1) (POTENTIAL).  
FT MOD\_RES 708 708 ALKYLATION (SH-2) (POTENTIAL).  
FT CONFLICT 15 15 A -> R (IN REF. 2).  
FT CONFLICT 970 970 E -> Q (IN REF. 1 AND 4).  
FT CONFLICT 1072 1072 M -> N (IN REF. 3).  
FT CONFLICT 1247 1247 N -> H (IN REF. 1 AND 4).  
FT CONFLICT 1251 1252 MC -> DGG (IN REF. 3).  
FT CONFLICT 1261 1261 E -> G (IN REF. 1 AND 4).  
FT CONFLICT 1297 1297 K -> Q (IN REF. 1 AND 4).  
FT CONFLICT 1377 1378 KY -> NT (IN REF. 3).  
FT CONFLICT 1504 1505 EN -> AH (IN REF. 1 AND 4).  
FT CONFLICT 1847 1847 E -> D (IN REF. 1 AND 4).  
FT CONFLICT 1914 1914 D -> H (IN REF. 2).  
SQ SEQUENCE 1937 AA; 222762 MW; A3EE2D51792E9E8 CRC64;

Query Match 14.88; Score 176.5; DB 1; Length 1937;  
Best Local Similarity 22.88; Pred. No. 0.045;  
Matches 84; Conservative 53; Mismatches 97; Indels 135; Gaps 13;

QY 5 DSM-----VQSLDVTAGFESYALPASIEDIKLSSIOEKAARAGKNAE----DVQ 54  
Db 1201 DSMAELGEOIDNLOVRKQLEKESELMETDLD-----SSNAEALISAKGLMEKMSLE 1256  
QY 55 HOILATESNOEYBMLDLOTKSALKETEL-----KEIVSFL-----OKIT 97  
Db 1257 DQVSELKTEEEQORLINDLTAQARALQTEAGEYSRQLEDERDALVSQLSRSKQASTQOIE 1316  
QY 98 DLONOLKQOEED-----FRKQLEDEGRKAEKENTTAELTEIEINKWRL 140  
Db 1317 ELKHQLEETKAKNALAHALQSSRHQDCLREQVEEEOGEKAEIQRLASANSVQAQRT 1376  
QY 141 LY-----EELYNKTKRPOIQLD-----APEVEKQALNE----- 169  
Db 1377 KYETDALQRTPEELEAKKLAORLOEAEHEVEAVNNAKASLEKTKORIQNEVEDLMQVE 1436  
QY 170 -HGAAPQLKKIRDSYAKLIGHQNLKQ-----KIKHYVK----- 202  
Db 1437 RSNAAACALDKKQRFNFKVLESEMKQYETQAELEASQKESRSLSTELFVKVNYESLD 1496  
QY 203 ----LNDENSOLKSEVSKLRQOLAK-----KKQ-----SEPKLOE 233  
Db 1497 QLETLRENNKNIQOEISDLTEQIABEGKQIHELEKTKKQYQOEKCEIQAALEENASLEH 1556  
QY 234 ELKKVVGIR 242  
Db 1557 EEGKILRIQ 1565

Search completed: July 17, 2003, 16:09:31  
Job time : 15 secs

